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DATE: 08/05/2002

PATENT APPLICATION: US/09/891,138A

TIME: 15:48:54

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1 <110> APPLICANT: Lin, Daniel Chi-Hong
2      Zhao, Jiagang
3      Chen, Jin-Long
4      Cutler, Gene
5      Tularik Inc.
6 <120> TITLE OF INVENTION: Novel Receptors
7 <130> FILE REFERENCE: 018781-006210US
8 <140> CURRENT APPLICATION NUMBER: US/09/891,138A
9 <141> CURRENT FILING DATE: 2001-06-25
10 <150> PRIOR APPLICATION NUMBER: US 60/213,461
11 <151> PRIOR FILING DATE: 2000-06-23
12 <160> NUMBER OF SEQ ID NOS: 26
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17 <212> TYPE: DNA
18 <213> ORGANISM: Mus musculus
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21 <222> LOCATION: (44)..(997)
22 <223> OTHER INFORMATION: mouse TGR18 G-protein coupled receptor (GPCR)
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47  tggtcaggtc gataagcgtg tttctgaaat agtcttattt ttattcttgt aatattaaaa 1440
48  tttatgtgaa aaatgaatat aattcaatgt acaacattag attttctatt tgaaaattat 1500
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61      20          25          30
62  Gly Leu Leu Gly Asn Val Thr Val Val Phe Gly Tyr Leu Phe Cys Met
63      35          40          45
64  Lys Asn Trp Asn Ser Ser Asn Val Tyr Leu Phe Asn Leu Ser Ile Ser
65      50          55          60
66  Asp Phe Ala Phe Leu Cys Thr Leu Pro Ile Leu Ile Lys Ser Tyr Ala
67      65          70          75          80
68  Asn Asp Lys Gly Thr Tyr Gly Asp Val Leu Cys Ile Ser Asn Arg Tyr
69      85          90          95
70  Val Leu His Thr Asn Leu Tyr Thr Ser Ile Leu Phe Leu Thr Phe Ile
71      100         105         110
72  Ser Met Asp Arg Tyr Leu Leu Met Lys Tyr Pro Phe Arg Glu His Phe
73      115         120         125
74  Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu Ala Val Trp Ala
75      130         135         140
76  Leu Val Thr Leu Glu Val Leu Pro Met Leu Thr Phe Ile Asn Ser Val
77      145         150         155         160
78  Pro Lys Glu Glu Gly Ser Asn Cys Ile Asp Tyr Ala Ser Ser Gly Asn
79      165         170         175
80  Pro Glu His Asn Leu Ile Tyr Ser Leu Cys Leu Thr Leu Leu Gly Phe
81      180         185         190
82  Leu Ile Pro Leu Ser Val Met Cys Phe Phe Tyr Tyr Lys Met Val Val
83      195         200         205
84  Phe Leu Lys Arg Arg Ser Gln Gln Gln Ala Thr Ala Leu Pro Leu Asp
85      210         215         220
86  Lys Pro Gln Arg Leu Val Val Leu Ala Val Val Ile Phe Ser Ile Leu
87      225         230         235         240
88  Phe Thr Pro Tyr His Ile Met Arg Asn Leu Arg Ile Ala Ser Arg Leu
89      245         250         255
90  Asp Ser Trp Pro Gln Gly Cys Thr Gln Lys Ala Ile Lys Ser Ile Tyr
91      260         265         270
92  Thr Leu Thr Arg Pro Leu Ala Phe Leu Asn Ser Ala Ile Asn Pro Ile
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94  Phe Tyr Phe Leu Met Gly Asp His Tyr Arg Glu Met Leu Ile Ser Lys

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110      agccgcgcgc tccgcctggt gttcctgggg gtcactctgg tggtagcggt ggcaggcaac 180
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112      aagatggact tcctgctggt gcagctggcc ctggcggacc tgtacgcgtg cgggggcacg 300
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115      gtgctcatcg cctcgcagcg ccggcgcgcg gtgcgtcttc cgcacggccg gccgctgccc 480
116      gcgcgtgccc tcgcgcctt gggtggctg ctggcactgc tgetggcgct gcccccgccc 540
117      ttcgtggtgc gcggggactc cccctgcgcg ctgccgcgcg cgcgcgcgcg aacgtccctg 600
118      cagccaggcg cgccccggc cgcccgcgcc tggccggggg agcgtcgtg ccacgggata 660
119      ttcgcgcccc tgccgcgtg gcacctgcag gtctacgctg tctacgaggg cgtcgcgggc 720
120      ttcgtcgcgc ctgttacggt cctgggcgtc gcttgcggcc acctactctc cgtctggtgg 780
121      cggcacccggc cgcaggcccc cgcggtgca gcgcctggt cggcgagccc aggtcgagcc 840
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128      cctcattatc accatgctcg gcgggaaccg ctggacgagg gcggcttgcg cccacccctt 1260
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135 <220> FEATURE:
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141          20          25          30
142      Gly Ala Pro Ala Ser Gly Pro Pro Ser Arg Arg Val Arg Leu Val Phe
143          35          40          45
144      Leu Gly Val Ile Leu Val Val Ala Val Ala Gly Asn Thr Thr Val Leu
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Input Set : N:\Crif3\07252002\I891138.raw

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148 Lys Met Asp Phe Leu Leu Val Gln Leu Ala Leu Ala Asp Leu Tyr Ala
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151 100 105 110
152 Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys Arg Phe Leu Gln Leu Leu
153 115 120 125
154 Gln Ala Ser Gly Arg Gly Ala Ser Ala His Leu Val Val Leu Ile Ala
155 130 135 140
156 Leu Glu Arg Arg Arg Ala Val Arg Leu Pro His Gly Arg Pro Leu Pro
157 145 150 155 160
158 Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu Leu Ala Leu Leu Leu Ala
159 165 170 175
160 Leu Pro Pro Ala Phe Val Val Arg Gly Asp Ser Pro Ser Pro Leu Pro
161 180 185 190
162 Pro Pro Pro Pro Pro Thr Ser Leu Gln Pro Gly Ala Pro Pro Ala Ala
163 195 200 205
164 Arg Ala Trp Pro Gly Glu Arg Arg Cys His Gly Ile Phe Ala Pro Leu
165 210 215 220
166 Pro Arg Trp His Leu Gln Val Tyr Ala Phe Tyr Glu Ala Val Ala Gly
167 225 230 235 240
168 Phe Val Ala Pro Val Thr Val Leu Gly Val Ala Cys Gly His Leu Leu
169 245 250 255
170 Ser Val Trp Trp Arg His Arg Pro Gln Ala Pro Ala Ala Ala Pro
171 260 265 270
172 Trp Ser Ala Ser Pro Gly Arg Ala Pro Ala Pro Ser Ala Leu Pro Arg
173 275 280 285
174 Ala Lys Val Gln Ser Leu Lys Met Ser Leu Leu Leu Ala Leu Leu Phe
175 290 295 300
176 Val Gly Cys Glu Leu Pro Tyr Phe Ala Ala Arg Leu Ala Ala Ala Trp
177 305 310 315 320
178 Ser Ser Gly Pro Ala Gly Asp Trp Glu Gly Glu Gly Leu Ser Ala Ala
179 325 330 335
180 Leu Arg Val Val Ala Met Ala Asn Ser Ala Leu Asn Pro Phe Val Tyr
181 340 345 350
182 Leu Phe Phe Gln Ala Gly Asp Cys Arg Leu Arg Arg Gln Leu Arg Lys
183 355 360 365
184 Arg Leu Gly Ser Leu Cys Cys Ala Pro Gln Gly Gly Ala Glu Asp Glu
185 370 375 380
186 Glu Gly Pro Arg Gly His Gln Ala Leu Tyr Arg Gln Arg Trp Pro His
187 385 390 395 400
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236      20          25          30
237      Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
238      35          40          45
239      Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
240      50          55          60
241      Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
242      65          70          75          80
243      Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
244      85          90          95
245      Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg

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